Amendments to the Claims are reflected in the listing of claims which begins on page 3 of this paper.

Remarks/Arguments begin on page 7 of this paper.

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A method of screening for ~~detecting~~ a splicing defect in a human dihydropyrimidine dehydrogenase gene wherein said gene comprises the sequence of SEQ ID NO:1 or the variant thereof wherein the residue at position 434 is an A and wherein said defect causes the exon of SEQ ID NO:1 to be skipped, said method comprising determining whether said gene has an A residue or a G residue at said position 434, wherein said method the presence of an A residue, but not a G residue, at said position 434 indicates the presence of the splicing defect causing the exon of SEQ ID NO:1 to be skipped. ~~the residue of a human genomic DNA encoding the human dihydropyrimidine dehydrogenase gene at the position indicated as nucleotide 434 of SEQ ID NO: 1 is a G residue or determining whether the residue at the position indicated as nucleotide 434 of SEQ ID NO: 1 is an A residue, wherein the substitution of the G residue with an A residue at position 434 causes the splicing defect in the human dihydropyrimidine dehydrogenase gene; and wherein the DNA, other than for any substitution of the G residue at position 434, comprises a nucleotide sequence identical to the sequence of residues 432-435 of SEQ ID NO: 1~~.

Claim 2 (currently amended): The method of claim 1, wherein the method comprises the step of amplifying a fragment of said gene comprising position 434 of SEQ ID NO:1 and detecting a G residue or an A residue at said position of said fragment. ~~human intronic dihydropyrimidine dehydrogenase genomic DNA to detect therein a G residue or an A residue at the position indicated as nucleotide 434 of SEQ ID NO: 1.~~

Claim 3 (currently amended): The method of claim 2, wherein the method comprises amplifying the fragment ~~genomic DNA~~ with a polymerase chain reaction primer from about 15 to about 20 nucleotides long and wherein said primer the nucleotides are in a sequence exactly complementary to a sequence of SEQ ID NO: 1 located between position 434 and 861.

Claim 4 (currently amended): The method of claim 2, wherein the detecting is by digestion of the amplified fragment ~~DNA~~ with a Mae II restriction endonuclease.

Claim 5 (previously presented): The method of claim 2, wherein the determining is by oligonucleotide array.

Claim 6 (currently amended): A method of screening a human ~~patients~~ for sensitivity to 5-fluorouracil, comprising:

(a) isolating genomic DNA from the human, said genomic DNA comprising the sequence of SEQ ID NO:1 or comprising the sequence of SEQ ID NO:1 wherein the residue at position 434 is an A;

(b) amplifying under stringent conditions a fragment of the genomic DNA comprising position 434 of SEQ ID NO:1; and

(c) determining whether the amplified fragment has an A or G residue at position 434; wherein the substitution of an A residue by a G residue at position 434 indicates the patient is sensitive to 5-fluorouracil.

~~isolating a genomic DNA from the patient, wherein the DNA comprises positions 432-435 of SEQ ID NO: 1; and determining whether a G residue is the nucleotide at position 434, and wherein the DNA, other than for any substitution of the G residue at position 434, comprises a nucleotide sequence identical to the sequence of residues 432-435 of SEQ ID NO: 1.~~

Claim 7 (cancelled).

Claim 8 (currently amended): The method of claim [[7]] 6, wherein the method comprises amplifying the genomic DNA with a polymerase chain reaction primer from about 15 to about 20 nucleotides long and wherein said primer the nucleotides are in a sequence exactly complementary to a sequence of SEQ ID NO: 1 located between position 434 and 861.

Claim 9 (currently amended): The method of claim [[7]] 6, wherein the determining is by digestion of the amplified DNA with a Mae II restriction endonuclease.

Claim 10 (currently amended): A composition comprising a polymerase chain reaction primer from about 15 to about 20 nucleotides long wherein said primer the nucleotide sequence is exactly complementary to a nucleotide sequence of SEQ ID NO: 1 located between position 434 and position 861.

Claim 11 (currently amended): The composition of claim 10, wherein said primer the nucleotides are in a sequence corresponding to a sequence of SEQ ID NO: 1 located between position 434 and position 534.

Claims 12-28 (cancelled).

Claim 29 (New): A method of testing a human for a single nucleotide polymorphism at position 434 of SEQ ID NO:1, the method comprising:

a) isolating a sample from the human of genomic DNA wherein the genomic DNA comprises the nucleotide sequence of SEQ ID NO:1 or the variant thereof wherein the nucleotide corresponding to position 434 of SEQ ID NO:1 is A;

b) selectively amplifying a fragment of the genomic DNA wherein the amplified fragment comprises position 434 of SEQ ID NO:1; and

c) determining whether the residue at position 434 of SEQ ID NO:1 is an A or a G.

Claim 30 (new): The method of claim 29, wherein the fragment of genomic DNA is amplified with a polymerase chain reaction primer from about 15 to about 20 nucleotides long and wherein said primer the nucleotides are in a sequence exactly complementary to a sequence of SEQ ID NO: 1 located between position 434 and 861.

Claim 31 (new): The method of claim 29, wherein the determining is by digestion of the amplified fragment with a Mae II restriction endonuclease.

Claim 32 (new): The method of claim 29, wherein the determining is by oligonucleotide array.

Claim 33 (new): A composition comprising a polymerase chain reaction primer from about 15 to about 20 nucleotides long wherein said primer the nucleotide sequence is exactly complementary to a nucleotide sequence of SEQ ID NO: 1 located between position 1 and position 268.

Claim 34 (new): A composition of claim 33, wherein the sequence of the primer is the sequence of SEQ ID NO:3.

Claim 35 (new): A composition of claim 10, wherein the sequence of the primer is the sequence of SEQ ID NO:4.

Claim 36 (new): The method of claim 29, wherein the residue at position 434 of SEQ ID NO:1 is an A.